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1998; No. 60/075,462 filed February 19, 1998; No. 60/075,461 filed February 19, 1998; No. 60/075,464 filed February 19, 1998; No. 60/075,460 filed February 19, 1998; No. 60/075,463 filed February 19, 1998; No. 60/077,231 filed March 9, 1998; No. 60/077,229 filed March 9, 1998; No. 60/077,230 filed March 9, 1998; No. 60/078,368 filed March 18, 1998; No. 60/080,844 filed April 7, 1998; No. 60/083,067 filed April 27, 1998; No. 60/083,387 filed April 29, 1998; No. 60/083,388 filed April 29, 1998; No. 60/085,224 filed May 13, 1998; No. 60/085,223 filed May 13, 1998; No. 60/085,222 filed May 13, 1998; No. 60/086,186 filed May 21, 1998; No. 60/086,187 filed May 21, 1998; No. 60/086,185 filed May 21, 1998; No. 60/086,184 filed May 21, 1998; No. 60/086,188 filed May 21, 1998; No. 60/089,524 filed June 16, 1998; No. 60/089,810 filed June 18, 1998; No. 60/089,814 filed June 18, 1998; No. 60/090,170 filed June 22, 1998; No. 60/092,036 filed July 8, 1998; No. 60/099,670 filed September 9, 1998; No. 60/099,697 filed September 9, 1998; No. 60/100,674 filed September 16, 1998; No. 60/101,132 filed September 21, 1998; No. 60/101,130 filed September 21, 1998; No. 60/101,508 filed September 22, 1998; No. 60/101,344 filed September 22, 1998; No. 60/101,347 filed September 22, 1998; No. 60/101,343 filed September 22, 1998; No. 60/104,126 filed October 13, 1998; No. 60/104,127 filed October 13, 1998; No. 60/104,124 filed October 13, 1998; No. 60/104,121 filed October 13, 1998; and No. 60/111,981 filed December 11, 1998 the disclosures of which applications are herein incorporated by reference in their entirety.

Please add the following heading and paragraph at page 2, line 5 following the section entitled "CROSS-REFERENCE TO RELATED APPLICATIONS" and prior to the "FIELD OF THE INVENTION":

INCORPORATION OF SEQUENCE LISTING

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A paper copy of the Sequence Listing and a computer readable form of the Sequence Listing on diskette, containing the file cytoseq2.txt, which is 393,815 bytes in size (measured in MS-DOS) and created on September 27, 2001, are herein incorporated by reference.

Please **replace** the paragraph at page 14, lines 5 to 21 with the following paragraph:

Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ) (www-ddbj.nig.ac.jp/); Genebank (www-ncbi.nlm.nih.gov/Web/Search/Index.html); and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) (www-ebi.ac.uk/ebi_docs/embl_db/embl_db.html). Other appropriate databases include dbEST (www-ncbi.nlm.nih.gov/dbEST/index.html), SwissProt (www-ebi.ac.uk/ebi_docs/swisprot_db/swisshome.html), PIR (www-nbrt.georgetown.edu/pir/) and The Institute for Genome Research (www-tigr.org/tdb/tdb.html).

Please **replace** the paragraph at page 16, lines 5 to 11 with the following paragraph:

Homologues in other organisms are available that can be used for comparative sequence analysis. Multiple alignments are performed to study similarities and differences in a group of related sequences. CLUSTAL W is a multiple sequence alignment package available that performs progressive multiple sequence alignments based on the method of Feng and Doolittle, *J. Mol. Evol.* 25: 351-360 (1987), the entirety of which is herein incorporated by reference. Each pair of sequences is aligned and the distance between each pair is calculated; from this distance matrix, a guide tree is calculated, and all of the sequences are progressively aligned based on this tree. A feature of the program is its sensitivity to the effect of gaps on the alignment; gap penalties are varied to encourage the insertion of gaps in probable loop regions instead of in the middle of structured regions. Users can specify gap penalties, choose between a number of scoring matrices, or supply their own scoring matrix for both the pairwise alignments and the multiple alignments. CLUSTAL W for UNIX and VMS systems is available by ftp at: ebi.ac.uk. Another program is MACAW (Schuler *et al.*, *Proteins, Struct. Func. Genet.* 9:180-190 (1991), the entirety of which is herein incorporated by reference), for which both Macintosh and Microsoft Windows versions are available.

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MACAW uses a graphical interface, provides a choice of several alignment algorithms, and is available by anonymous ftp at: [ncbi.nlm.nih.gov \(directory/pub/macaw\)](ftp://ncbi.nlm.nih.gov/directory/pub/macaw).

Please **delete** the paragraph at page 48, lines 11 to 17, and replace it with the following paragraph:

By

A PCR probe is a nucleic acid molecule capable of initiating a polymerase activity while in a double-stranded structure with another nucleic acid. Various methods for determining the structure of PCR probes and PCR techniques exist in the art. Computer generated searches using programs such as Primer3 (available on the World Wide Web at genome.wi.mit.edu/cgi-bin/primer/primer3.cgi), STSPipeline (available on the World Wide Web at genome.wi.mit.edu/cgi-bin/www-STSPipeline) or GeneUp (Pesole *et al.*, *BioTechniques* 25:112-123 (1998) the entirety of which is herein incorporated by reference), for example, can be used to identify potential PCR primers.
